



Figure 5-figure supplement 3 TRAVs are used to different extents by naïve CD4 T cells in mice expressing different MHCII alleles and/or different TCRβs. Data were obtained and analyzed as described in Figures 3 and 5. DESeq 2 was used to compare the frequencies with which different TRAVs were used by naïve CD4 T cells in mice expressing different MHCII alleles and/or different TCRβs. Differential expression analyses were performed using the DESeq2 package (v1.8.1) in the R language (v3.2.2). DESeq2 fit negative binomial regression models to each feature to compare between groups. Corrections for size factors for each sample (animal) to account for differences in repertoire size were applied. The negative binomial dispersion parameter for each feature was then calculated, sharing information across features with similar expression levels to moderate extreme empirical dispersion estimates. Wald tests were applied to each feature to test for differential expression between groups. Features were considered differentially expressed if they had a Benjamini-Hochberg adjusted p-value (i.e., false discovery rate) <0.05.